

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,369  
Source: JFWP  
Date Processed by STIC: 1-23-06

***ENTERED***



IFWP

**RAW SEQUENCE LISTING** DATE: 01/23/2006  
**PATENT APPLICATION:** US/10/564,369 TIME: 09:55:55

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF4\01232006\J564369.raw

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3 <110> APPLICANT: Oregon Health & Science University
4      Moses, Ashlee
5      Nelson, Jay
6      Fruh, Klaus
7      King, Jeff
8      Jelinek, Laura
9      Hirsch, Alec
10     DeFilippis, Victor
12 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS USING
MODULATORS OF
13     VIRUS-INDUCED CELLULAR GENE SEQUENCES
15 <130> FILE REFERENCE: 899-73077-04
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/564,369
C--> 18 <141> CURRENT FILING DATE: 2006-01-11
20 <150> PRIOR APPLICATION NUMBER: PCT/US2004/011988
21 <151> PRIOR FILING DATE: 2004-04-15
23 <150> PRIOR APPLICATION NUMBER: US 60/486,694
24 <151> PRIOR FILING DATE: 2003-07-11
26 <150> PRIOR APPLICATION NUMBER: US 60/533,103
27 <151> PRIOR FILING DATE: 2003-12-29
29 <160> NUMBER OF SEQ ID NOS: 17
31 <170> SOFTWARE: PatentIn version 3.2
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1232
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (19)..(1044)
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45             Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro
46             1           5           10
48 acg gaa aag cag cgg tac ctg gat gag gcc gag aga gag aag cag cag      99
49 Thr Glu Lys Gln Arg Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln
50             15          20          25
52 tac atg aag gag ctg cgg gcg tac cag cag tct gaa gcc tat aag atg    147
53 Tyr Met Lys Glu Leu Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met
54             30          35          40
56 tgc acg gag aag atc cag gag aag aac atc aag aaa gaa gac tcg agc    195
57 Cys Thr Glu Lys Ile Gln Glu Lys Ile Lys Lys Glu Asp Ser Ser
58             45          50          55
60 tct ggg ctc atg aac act ctc ctg aat gga cac aag ggt ggg gac tgc    243
61 Ser Gly Leu Met Asn Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys

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62	60	65	70	75	
64	gat ggc ttc tcc acc ttc gat gtt ccc atc ttc act gaa gag ttc ttg				291
65	Asp Gly Phe Ser Thr Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu				
66	80	85	90		
68	gac caa aac aaa gcg cgt gag gcg gag ctt cgg cgc ttg cgg aag atg				339
69	Asp Gln Asn Lys Ala Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met				
70	95	100	105		
72	aat gtg gcc ttc gag gag cag aac gcg gta ctg cag agg caa aac gca				387
73	Asn Val Ala Phe Glu Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala				
74	110	115	120		
76	gag cat gag cag cgc gcg cga gcg tct gga gca gga gct ggc gct gga				435
77	Glu His Glu Gln Arg Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly				
78	125	130	135		
80	gga gcg gag gac gct ggc gct gca gca gca gct cca ggc cgt gcg cca				483
81	Gly Ala Glu Asp Ala Gly Ala Ala Ala Ala Pro Gly Arg Ala Pro				
82	140	145	150	155	
84	ggc gct cac cgc cag ctt cgc ctc act gcc ggt gcc ggg cac ggg cga				531
85	Gly Ala His Arg Gln Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg				
86	160	165	170		
88	aac gcc cac gct ggg cac tct gga ctt cta cat ggc ccg gct tca cgg				579
89	Asn Ala His Ala Gly His Ser Gly Leu Leu His Gly Pro Ala Ser Arg				
90	175	180	185		
92	agc cat cga gcg cga ccc cgc cca gca cga gaa gct cat cgt ccg cat				627
93	Ser His Arg Ala Arg Pro Arg Pro Ala Arg Glu Ala His Arg Pro His				
94	190	195	200		
96	caa gga aat cct ggc cca ggt cgc cag cga gca cct gtg agg agt ggg				675
97	Gln Gly Asn Pro Gly Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly				
98	205	210	215		
100	cgg gcc cac gat gca gag gag aag ctg tgg gcg cgg ccc tgc cac acc				723
101	Arg Ala His Asp Ala Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr				
102	220	225	230	235	
104	cca ccc cgt gga cga gag gct ggg ggt cca ccc ttt ggg gcc tgg tcc				771
105	Pro Pro Arg Gly Arg Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser				
106	240	245	250		
108	cat cct gca cct ttg ggg gct cca gcc ccc cta aaa tta aat ttc tgc				819
109	His Pro Ala Pro Leu Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys				
110	255	260	265		
112	agc atc cct tta gct ttc aat ctc ccc agc ccc ctg aac ccg gaa aaa				867
113	Ser Ile Pro Leu Ala Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys				
114	270	275	280		
116	gca ctc gct gcg cga tac acc cag aag aac ctc aca gcc gag ggt gcc				915
117	Ala Leu Ala Ala Arg Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala				
118	285	290	295		
120	cct cct cggt agg aca gcc acg cgc tac act ggc tct ccg ggc cac ccc				963
121	Pro Pro Arg Arg Thr Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro				
122	300	305	310	315	
124	cag gac aca ggg cag acg aaa ccc acc ccc agc aca ccg cag gac ccc				1011
125	Gln Asp Thr Gly Gln Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro				
126	320	325	330		

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128 cca aat tac tca cta cgg gct gtg cca tag gccacacagg aagctgcctt 1064
129 Pro Asn Tyr Ser Leu Arg Gly Ala Val Pro
130 335 340
132 gtggggactt acctgggtg tccccgcat gcctgtaccc cagatgggtg ggggccggct 1124
134 ttgcccattc tgctctcctc cagccgaggg accctggtgg gggtggctcc ttctcactgc 1184
136 tggatccgga ctttttaat aaaaacaagt aaaatttgtg ttttaaaa 1232
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 341
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
146 Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro Thr Glu Lys Gln Arg
147 1 5 10 15
150 Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln Tyr Met Lys Glu Leu
151 20 25 30
154 Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met Cys Thr Glu Lys Ile
155 35 40 45
158 Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser Gly Leu Met Asn
159 50 55 60
162 Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys Asp Gly Phe Ser Thr
163 65 70 75 80
166 Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu Asp Gln Asn Lys Ala
167 85 90 95
170 Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met Asn Val Ala Phe Glu
171 100 105 110
174 Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala Glu His Glu Gln Arg
175 115 120 125
178 Ala Arg Ala Ser Gly Ala Gly Ala Gly Gly Ala Glu Asp Ala
179 130 135 140
182 Gly Ala Ala Ala Ala Pro Gly Arg Ala Pro Gly Ala His Arg Gln
183 145 150 155 160
186 Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly
187 165 170 175
190 His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg
191 180 185 190
194 Pro Arg Pro Ala Arg Glu Ala His Arg Pro His Gln Gly Asn Pro Gly
195 195 200 205
198 Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly Arg Ala His Asp Ala
199 210 215 220
202 Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr Pro Pro Arg Gly Arg
203 225 230 235 240
206 Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu
207 245 250 255
210 Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala
211 260 265 270
214 Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys Ala Leu Ala Ala Arg
215 275 280 285
218 Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala Pro Pro Arg Arg Thr
219 290 295 300

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222 Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro Gln Asp Thr Gly Gln  
223 305 310 315 320  
226 Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro Pro Asn Tyr Ser Leu  
227 325 330 335  
230 Arg Gly Ala Val Pro  
231 340  
234 <210> SEQ ID NO: 3  
235 <211> LENGTH: 3870  
236 <212> TYPE: DNA  
237 <213> ORGANISM: Homo sapiens  
240 <220> FEATURE:  
241 <221> NAME/KEY: CDS  
242 <222> LOCATION: (179) .. (1642)  
244 <400> SEQUENCE: 3  
245 caggagaca tacaggattt aagaagccca tcatggagaa gacccat tacagagata 60  
247 aaaagtttt ctgttggAAC aagttaaacAC tagatggcAG ataacagACT gaggagtGAG 120  
249 ctgcttctGA ctcgattaaa aagggagtGA gccataactG gcggctgctC ttgcGCCA 178  
251 atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag 226  
252 Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu  
253 1 5 10 15  
255 ggc aac aag acc act atg gcc agc ccc cag ctg atg ccc ctg gtG gtG 274  
256 Gly Asn Lys Thr Thr Met Ala Ser Pro Gln Leu Met Pro Leu Val Val  
257 20 25 30  
259 gtc ctg agc act atc tgc ttG gtc aca gta ggg ctc aac ctg ctg gtG 322  
260 Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val  
261 35 40 45  
263 ctg tat gca gta cgg agt gag cgg aag ctc cac act gtG ggg aac ctg 370  
264 Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu  
265 50 55 60  
267 tac atc gtc agc ctc tcG gtG gcg gac ttG atc gtG ggt gcc gtc gtc 418  
268 Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val  
269 65 70 75 80  
271 atg cct atg aac atc ctc tac ctG ctc atg tcc aag tgg tca ctG ggc 466  
272 Met Pro Met Asn Ile Leu Tyr Leu Leu Met Ser Lys Trp Ser Leu Gly  
273 85 90 95  
275 cgt cct ctc tgc ctc ttt tgg ctt tcc atg gac tat gtG gcc agc aca 514  
276 Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr  
277 100 105 110  
279 gcg tcc att ttc agt gtc ttc atc ctG tgc att gat cgc tac cgc tct 562  
280 Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser  
281 115 120 125  
283 gtc cag cag ccc ctc agg tac ctt aag tat cgt acc aag acc cga ggc 610  
284 Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala  
285 130 135 140  
287 tcg gcc acc att ctG ggg gcc tgg ttt ctc tct ttt ctG tgg gtt att 658  
288 Ser Ala Thr Ile Leu Gly Ala Trp Phe Leu Ser Phe Leu Trp Val Ile  
289 145 150 155 160  
291 ccc att cta ggc tgg aat cac ttc atg cag cag acc tcG gtG cgc cga 706  
292 Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg

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293	165	170	175	
295	gag gac aag tgt gag aca gac ttc tat gat gtc acc tgg ttc aag gtc			754
296	Glu Asp Lys Cys Glu Thr Asp Phe Tyr Asp Val Thr Trp Phe Lys Val			
297	180	185	190	
299	atg act gcc atc atc aac ttc tac ctg ccc acc ttg ctc atg ctc tgg			802
300	Met Thr Ala Ile Ile Asn Phe Tyr Leu Pro Thr Leu Leu Met Leu Trp			
301	195	200	205	
303	ttc tat gcc aag atc tac aag gcc gta cga caa cac tgc cag cac cgg			850
304	Phe Tyr Ala Lys Ile Tyr Lys Ala Val Arg Gln His Cys Gln His Arg			
305	210	215	220	
307	gag ctc atc aat agg tcc ctc cct tcc tca gaa att aag ctg agg			898
308	Glu Leu Ile Asn Arg Ser Leu Pro Ser Phe Ser Glu Ile Lys Leu Arg			
309	225	230	235	240
311	cca gag aac ccc aag ggg gat gcc aag aaa cca ggg aag gag tct ccc			946
312	Pro Glu Asn Pro Lys Gly Asp Ala Lys Lys Pro Gly Lys Glu Ser Pro			
313	245	250	255	
315	tgg gag gtt ctg aaa agg aag cca aaa gat gct ggt ggt gga tct gtc			994
316	Trp Glu Val Leu Lys Arg Lys Pro Lys Asp Ala Gly Gly Ser Val			
317	260	265	270	
319	ttg aag tca cca tcc caa acc ccc aag gag atg aaa tcc cca gtt gtc			1042
320	Leu Lys Ser Pro Ser Gln Thr Pro Lys Glu Met Lys Ser Pro Val Val			
321	275	280	285	
323	ttc agc caa gag gat gat aga gaa gta gac aaa ctc tac tgc ttt cca			1090
324	Phe Ser Gln Glu Asp Asp Arg Glu Val Asp Lys Leu Tyr Cys Phe Pro			
325	290	295	300	
327	ctt gat att gtg cac atg cag gct gcg gca gag ggg agt agc agg gac			1138
328	Leu Asp Ile Val His Met Gln Ala Ala Glu Gly Ser Ser Arg Asp			
329	305	310	315	320
331	tat gta gcc gtc aac cgg agc cat ggc cag ctc aag aca gat gag cag			1186
332	Tyr Val Ala Val Asn Arg Ser His Gly Gln Leu Lys Thr Asp Glu Gln			
333	325	330	335	
335	ggc ctg aac aca cat ggg gcc agc gag ata tca gag gat cag atg tta			1234
336	Gly Leu Asn Thr His Gly Ala Ser Glu Ile Ser Glu Asp Gln Met Leu			
337	340	345	350	
339	ggt gat agc caa tcc ttc tct cga acg gac tca gat acc acc aca gag			1282
340	Gly Asp Ser Gln Ser Phe Ser Arg Thr Asp Ser Asp Thr Thr Glu			
341	355	360	365	
343	aca gca cca ggc aaa ggc aaa ttg agg agt ggg tct aac aca ggc ctg			1330
344	Thr Ala Pro Gly Lys Gly Lys Leu Arg Ser Gly Ser Asn Thr Gly Leu			
345	370	375	380	
347	gat tac atc aag ttt act tgg aag agg ctc cgc tcg cat tca aga cag			1378
348	Asp Tyr Ile Lys Phe Thr Trp Lys Arg Leu Arg Ser His Ser Arg Gln			
349	385	390	395	400
351	tat gta tct ggg ttg cac atg aac cgc gaa agg aag gcc gcc aaa cag			1426
352	Tyr Val Ser Gly Leu His Met Asn Arg Glu Arg Lys Ala Ala Lys Gln			
353	405	410	415	
355	ttg ggt ttt atc atg gca gcc ttc atc ctc tgc tgg atc cct tat ttc			1474
356	Leu Gly Phe Ile Met Ala Ala Phe Ile Leu Cys Trp Ile Pro Tyr Phe			
357	420	425	430	

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/564,369

DATE: 01/23/2006  
TIME: 09:55:56

Input Set : A:\sequence listing.txt  
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L:17 M:270 C: Current Application Number differs, Wrong Format  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date